

## SUBSTITUTE SEQUENCE LISTING

&lt;110&gt; RIKEN

&lt;120&gt; Truncated Reelin Protein and DNA Encoding the Same

&lt;130&gt; PH-1167

&lt;140&gt; US 09/882,189

&lt;141&gt; 2001-04-11

&lt;150&gt; JP 2000-109954

&lt;151&gt; 2000-04-11

&lt;160&gt; 28

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 2274

&lt;212&gt; DNA

&lt;213&gt; Xenopus laevis

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&lt;221&gt; misc\_feature

&lt;222&gt; (100)

&lt;223&gt; a or g or t or c

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&lt;221&gt; CDS

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&lt;222&gt; (157)..(234)

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&lt;222&gt; (241)..(726)

&lt;223&gt; F-spondin domain

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&lt;222&gt; (847)..(1197)

&lt;223&gt; CR-50 epitope region

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Gly Asn Pro Ser Tyr Tyr Ile Pro Gly Gln Glu Tyr His Val Thr Ile  
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Gly Phe Gly Ile Met Ser Asp Arg Gln Phe Gly Thr Gln Phe Met Cys  
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Asn Leu Ala Glu Ile His Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe  
195 200 205  
Asp Ser Tyr Lys Leu Gln Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys  
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225 230 235 240  
Ala Val Thr Phe Cys Asp Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val  
245 250 255  
Gln Met Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser  
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Thr Lys Asn Asn Ser Ser Ser Trp Met Pro Leu Glu Arg Ile Ser Ala  
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Sub  
B1  
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 Ile Asn Ala Ala His Lys Glu Val Val Leu Glu Asp Asn Leu Asp Pro  
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 Met Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His  
 370 375 380  
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 385 390 395 400  
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 Met Glu Arg Gly  
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tgc tgg gcg ccg cgg gct ctc gtc ctg gcc gtg ctg ctg ctg ctg gcg 342  
 Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu Leu Leu Leu Ala  
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Thr	Leu	Arg	Ala	Arg	Ala	Ala	Thr	Gly	Tyr	Tyr	Pro	Arg	Phe	Ser	Pro	
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Phe	Phe	Phe	Leu	Cys	Thr	His	His	Gly	Glu	Leu	Glu	Gly	Asp	Gly	Glu	
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Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu Glu  
35 40 45

Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly  
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Asn Pro Thr Tyr Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser  
65 70 75 80

Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser

Sub  
B1  
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Val	Val	Ala	Ser	His	Val	Ser	His	Leu	Pro	Thr	Thr	Asn	Leu	Ser	Phe				
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Val	Trp	Ile	Ala	Pro	Pro	Ala	Gly	Thr	Gly	Cys	Val	Asn	Phe	Met	Ala				
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Thr	Ala	Thr	His	Arg	Gly	Gln	Val	Ile	Phe	Lys	Asp	Ala	Leu	Ala	Gln				
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Gln	Leu	Cys	Glu	Gln	Gly	Ala	Pro	Thr	Glu	Ala	Thr	Ala	Tyr	Ser	His				
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Leu	Ala	Glu	Ile	His	Ser	Asp	Ser	Val	Ile	Leu	Arg	Asp	Asp	Phe	Asp				
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Ser	Tyr	Gln	Gln	Leu	Glu	Leu	Asn	Pro	Asn	Ile	Trp	Val	Glu	Cys	Ser				
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Leu	Asn	Thr	Thr	Thr	Ala	Ser	Val	Leu	Gln	Phe	Ser	Ile	Gly	Ser	Gly				
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Ser	Cys	Arg	Phe	Ser	Tyr	Ser	Asp	Pro	Ser	Ile	Thr	Val	Ser	Tyr	Ala				
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Lys	Asn	Asn	Thr	Ala	Asp	Trp	Ile	Gln	Leu	Glu	Lys	Ile	Arg	Ala	Pro				
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Ser	Asn	Val	Ser	Thr	Val	Ile	His	Ile	Leu	Tyr	Leu	Pro	Glu	Glu	Ala				
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Lys	Gly	Glu	Ser	Val	Gln	Phe	Gln	Trp	Lys	Gln	Asp	Ser	Leu	Arg	Val				
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Gly	Glu	Val	Tyr	Glu	Ala	Cys	Trp	Ala	Leu	Asp	Asn	Ile	Leu	Val	Ile				
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Asn	Ser	Ala	His	Arg	Glu	Val	Val	Leu	Glu	Asp	Asn	Leu	Asp	Pro	Val				
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Cys	Gln	Ser	Asp	Gly	Asn	Ser	Ile	Tyr	Phe	His	Gly	Asn	Glu	Gly	Ser				
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Glu	Phe	Asn	Phe	Ala	Thr	Thr	Arg	Asp	Val	Asp	Leu	Ser	Thr	Glu	Asp				
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Ile	Gln	Glu	Gln	Trp	Ser	Glu	Glu	Phe	Glu	Ser	Gln	Pro	Thr	Gly	Trp				
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 465 470 475 480  
 Met Gly Gly Ile Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile  
 485 490 495  
 Leu Tyr Ala Lys Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr  
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 Leu Thr Tyr Ser Ser Tyr Lys Val Pro Ser Leu Val Ser Val Val Ile  
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 530 535 540  
 Ser His Gln Gly Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His  
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